SEQUENCE LISTING

<110> Oklahoma Medical Research Foundation
       Sauer, Brian Lee
       Rufer, Andreas Walter

<120> Method for Selecting Recombinase Variants with Altered Specificity

<130> OMRF 178

<140> 09/544,045
<141> 2000-04-06

<150> 60/127,977
<151> 1999-04-06

<160> 68

<170> PatentIn version 3.1

<210> 1
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Cre

<400> 1

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35   40   45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50   55   60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65   70   75   80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
            85   90   95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100   105   110

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Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
        130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
            165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
        210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
            245                 250                 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
            325                 330                 335
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Arg Leu Leu Glu Asp Gly Asp
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<210> 2
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> Inverted repeat sequence

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<221> misc_feature
<222> (1)..(3)
<223> N at positions 1-3 can be A, T, G, or C.

<220>
<221> misc_feature
<222> (6)..(7)
<223> N at positions 6 and 7 can be A, T, G, or C.

<400> 2
nnnacnncgt ata

<210> 3
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> variant lox sites

<220>
<221> misc_feature
<222> (1)..(3)
<223> N at postitions 1-3 can be A, G, C, or T

<220>
<221> misc_feature
<222> (6)..(7)
<223> N at positions 6 and 7 can be A, T, G, C,

<220>
<221> misc_feature
<222> (14)..(21)
<223> N at positions 14-21 can A, G, T, or C

<220>
<221> misc_feature
<222> (28)..(29)

<223>   N at postions 28 and 29 can be A, T, G, or C

<220>
<221> misc_feature
<222> (32)..(34)
<223>   N at postiions 32-34 can be A, T, G, or C

<400> 3
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<210> 4
<211> 33
<212> DNA
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<220>
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<400> 4
gatacaacgt atataccttt ctatacgttg tat   33

<210> 5
<211> 34
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<220>
<223> Specific and non-specific sequences for Cre recombinase

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<223>   N at postions 1-3 can be A, T, G, or C

<220>
<221> misc_feature
<222> (14)..(21)
<223>   N at positions 14-21 can be A, T, C, or G

<220>
<221> misc_feature
<222> (32)..(34)
<223>   N at positions 32-34 can be A, T, G, or C

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<210> 6
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<212>   PRT
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<220>
<223>   oligonucleotide

<400>   6

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<210>   7
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<220>
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<220>
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<400>   8
aaataatcta gactgagtgt gaaatgtcc                                          29


<210>   9
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<212>   DNA
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<220>
<223>   primer

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<400>   10
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ataagcggcc gctgagcttg gctgttttgg cgg   33

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gccgtctcga gagagtttgt agaaacgcaa aaaggc   36

<210> 12
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<212> DNA
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<223> primer

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gtcaagctag ctagcaggtt tcccgactgg   30

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<220>
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acattgcggc cgcagatctc ctctagagtc gacctg   36

<210> 14
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<220>
<223> primer

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tttgggctag cgaattcgag   20

<210> 15
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<220>

<223> primer

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<210> 16
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<220>
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<400> 16
cggtgggaga atgttaatcc   20

<210> 17
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<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 17
ggacacagtg cccgtgtc   18

<210> 18
<211> 21
<212> DNA
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<220>
<223> primer

<400> 18
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<210> 19
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<220>
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<400> 19
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<210> 20
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<212> DNA

<213>   artificial sequence

<220>
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<210>   21
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<210>   22
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<212>   DNA
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<400>   22
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<212>   DNA
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<400>   23
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<210>   24
<211>   45
<212>   DNA
<213>   artificial sequence

<220>
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<223>  primer

<400>  25
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<210>  26
<211>  45
<212>  DNA
<213>  artificial sequence

<220>
<223>  primer

<220>
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<222>  (17)..(25)
<223>  N at positions 17-25 can be A, T, G, or C


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<210>  27
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<212>  DNA
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<223>  primer

<220>
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<222>  (17)..(25)
<223>  N at positions 17-25 can be A, T, G, or C


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gagttgcttc aaaaatnnnn nnnnnggcgc gagttgatag ctggc          45


<210>  28
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<212>  DNA
<213>  artificial sequence

<220>
<223>  wtCre

<400>  28
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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg     180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa     240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg     300

tctggcagta aaaactatcc agcaacattt gggccagcta acatgcttc atcgtcggtc      360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa     420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt     480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc     540

atttctgggg attgcttata caccctgtt acgtatagcc gaaattgcca ggatcagggt      600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac     660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga     720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt     780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctgga     840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag     900

atacctggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc     960

tggagtttca ataccggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat    1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg    1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt    1140

tcagcctgat acagattaaa tcagaacgca ga                                   1172


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<223>   mxoxox1

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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga     120

ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg     180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa     240
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atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg       300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc       360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa       420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt       480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc       540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt       600

taaagatatc tcacgtacta acggtgggag aatgttaatc catattggca gaacgaaaac       660

gctggttagc accgcaggtg tagagaaggc acttagtctg ggggtaacta aactggtcga       720

gcgatggatt tccatctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt       780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg       840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag       900

atacctggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc       960

tggagtttca ataccggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat      1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg      1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt      1140

tcagcctgat acagattaaa tcagaacgca ga                                    1172


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<212>   DNA
<213>   artificial sequence

<220>
<223>   mxoxox2

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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga       120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg       180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa       240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg       300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc       360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa       420
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agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcggac gcactgattt    480

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atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt    600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac    660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga    720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt    780

cagaaaaaat ggtgttgccg cgccatctgc caccggccag ctatcaactc gcgccctggg    840

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atacctggcc tggtccggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc    960

tggagtttca ataccggaga tcatgcaagc tggtggctgg tccaatgtaa atattgtcat   1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg   1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt   1140

tcagcctgat acagattaaa tcagaacgca ga                                1172


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<220>
<223>   mxoxox3

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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg    180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa    240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg    300

tctggcagta aaaactatcc agcaacattt gggccagcta acatgcttc atcgtcggtc     360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatcggc ggatccgaaa     420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt    480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc    540

atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt    600

taaagatatc tcacgtacta acggtgggag aatgttaatc catattagca gaacgaaaac    660
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gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga   720

gcaatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt   780

cagaaaaaat ggtgttgccg cgccatctgc caccagccgg ctatcaactc gcgccctggg   840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag   900

atacctggcc tggtccggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc   960

tggagtttca atactggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat   1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg   1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt   1140

tcagcctgat acagattaaa tcagaacgca ga   1172

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ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg   180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa   240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatgtcttc aggcgcgcgg   300

tctggcagta aaaactatcc agcaacattt gggccagcta acatgcttc atcgtcggtc   360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa   420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcaaac gcactgattt   480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc   540

atttctgggg attgcttata caccctgtt acgtatagcc gaaattgcca ggatcagggt   600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac   660

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gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt   780

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tggagtttca ataccggaga tcatgcaagc tggtggctgg accaatgtaa atattgtcat      1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg      1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt      1140

tcagcctgat acagattaaa tcagaacgca ga                                    1172
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<400>   33

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ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg       180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa       240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg       300

tctggcagta aaaactatcc agcaacattt gggccagcta acatgcttc atcgtcagtc        360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa       420

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atacctggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc       960

tggagtttca ataccggaga tcatgcaagc tggtggctgg tccaatgtaa atattgtcat      1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg      1080
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tcagcctgat acagattaaa tcagaacgca ga                                  1172


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caatttactg accgtacacc aaaatttgcc tgcattaccg gtcgatgcaa cgagtgatga     120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg     180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa     240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg     300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc     360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa     420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt     480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc     540

atttctgggg attgcttata caccctgtt acgtatagcc gaaattgcca ggatcagggt      600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac     660

gctggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga     720

gcgatggatt ccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt      780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg     840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag     900

ataccaggcc tggtctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc     960

tggagtttca ataccggaga tcatgcaagc tggtggctgg tccaatgtaa atattgtcat    1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg    1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt    1140

tcagcctgat acagattaaa tcagaacgca ga                                  1172


<210>   35
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<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox1

<400> 35

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1   5   10   15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
            20   25   30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
            35   40   45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
        50   55   60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65   70   75   80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85   90   95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100   105   110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115   120   125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
        130   135   140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145   150   155   160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165   170   175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
            180   185   190

```
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
        195             200             205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
        210             215             220

Ile Ser Ile Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225             230             235             240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
            245             250             255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
        260             265             270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275             280             285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290             295             300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305             310             315             320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
            325             330             335

Arg Leu Leu Glu Asp Gly Asp
            340


<210>   36
<211>   343
<212>   PRT
<213>   artificial sequence

<220>
<223>   mxoxox2

<400>   36

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5               10              15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20              25              30
```

```
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
     35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
     50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                 85                  90                  95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
              100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
         115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Gly Arg Thr Asp Phe Asp Gln
    130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
              165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
              180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
         195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Gly Gln Leu
              245                 250                 255
```

```
Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
        260              265                  270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275              280                  285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
        290              295                  300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305              310                  315                  320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                  330                  335

Arg Leu Leu Glu Asp Gly Asp
        340


<210>   37
<211>   343
<212>   PRT
<213>   artificial sequence

<220>
<223>   mxoxox3

<400>   37

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Ile
1               5                   10                  15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35                  40                  45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65                  70                  75                  80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95
```

```
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100                 105                 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
            115                 120                 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
            130                 135                 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
                165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
                180                 185                 190

Met Leu Ile His Ile Ser Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
            195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Gln Trp
            210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Arg Leu
                245                 250                 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
            275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295                 300

Ser Ile Leu Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320
```

```
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335


Arg Leu Leu Glu Asp Gly Asp
            340


<210>   38
<211>   343
<212>   PRT
<213>   artificial sequence

<220>
<223>   mxoxox4

<400>   38

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5                   10                  15


Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20                  25                  30


Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
            35                  40                  45


Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50                  55                  60


Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Cys Leu Gln Ala
65                  70                  75                  80


Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85                  90                  95


Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
                100                 105                 110


Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
            115                 120                 125


Glu Arg Ala Lys Gln Ala Leu Ala Phe Lys Arg Thr Asp Phe Asp Gln
            130                 135                 140


Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145                 150                 155                 160
```

```
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
              165                 170                 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
              180                 185                 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
              195                 200                 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
       210                 215                 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225                 230                 235                 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
              245                 250                 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
              260                 265                 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
              275                 280                 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
       290                 295                 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305                 310                 315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
              325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
              340


<210>   39
<211>   343
<212>   PRT
<213>   artificial sequence

<220>
<223>   mxoxox5
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<400> 39

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1   5   10   15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
            20   25   30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35   40   45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50   55   60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65   70   75   80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
            85   90   95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
            100   105   110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
        115   120   125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130   135   140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145   150   155   160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
            165   170   175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
        180   185   190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
    195   200   205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Gln Val Glu Arg Trp
    210   215   220

```
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225             230             235             240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
                245             250             255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260             265             270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
        275             280             285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290             295             300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
305             310             315             320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
            325             330             335

Arg Leu Leu Glu Asp Gly Asp
            340


<210>   40
<211>   343
<212>   PRT
<213>   artificial sequence

<220>
<223>   mxoxox6

<400>   40

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1               5               10              15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
            20              25              30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
        35              40              45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
    50              55              60
```

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65   70   75   80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
                85   90   95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
                100   105   110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
            115   120   125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
    130   135   140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145   150   155   160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
            165   170   175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
            180   185   190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
    195   200   205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
    210   215   220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225   230   235   240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
            245   250   255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
            260   265   270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
    275   280   285

```
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
    290                 295             300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
305                 310             315                 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
                325                 330                 335

Arg Leu Leu Glu Asp Gly Asp
            340
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<210>   41
<211>   13
<212>   DNA
<213>   artificial sequence

<220>
<223>   loxP

<220>
<221>   misc_feature
<222>   (6)..(7)
<223>   nn is either TT, TG, GT, GG, TC, CC, or AA


<400>   41
ataacnncgt ata                                                    13


<210>   42
<211>   13
<212>   DNA
<213>   artificial sequence

<220>
<223>   loxK2

<400>   42
ataacaacgt ata                                                    13


<210>   43
<211>   13
<212>   DNA
<213>   artificial sequence

<220>
<223>   loxK1

<400>   43
ataicctttgt ata                                                   13
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<210> 44
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxP

<400> 44
ataacttcgt atatacccttt ctatagcaag ttat   34

<210> 45
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2

<400> 45
ataacaacgt atatacccttt ctatagcttg ttat   34

<210> 46
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK1

<400> 46
atacctttgt atatacccttt ctatagaaag gtat   34

<210> 47
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GG'

<400> 47
ataacggcgt atatacccttt ctatagcccg ttat   34

<210> 48
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'CC'

<400> 48
ataaccccgt atataccttt ctatagcggg ttat   34

<210> 49
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TC'

<400> 49
ataactccgt atataccttt ctatagcgag ttat   34

<210> 50
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GT'

<400> 50
ataacgtcgt atataccttt ctatagcacg ttat   34

<210> 51
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TG'

<400> 51
ataactgcgt atataccttt ctatagccag ttat   34

<210> 52
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> LoxP

<400> 52
ataacttcgt ataatgtatg ctatacgaag ttat   34

<210> 53
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223>   LoxK1

<400>   53
gagcctttgt atataccttt ctatacaaag gctt   34

<210>   54
<211>   34
<212>   DNA
<213>   artificial sequence

<220>
<223>   loxK2

<400>   54
gatacaacgt atataccttt ctatacgttg tatt   34

<210>   55
<211>   64
<212>   DNA
<213>   artificial sequence

<220>
<223>   Gene

<400>   55
gctagcgaat tcgagcttcg gtacccgggg atcctctaga gtcgacctgc aggcatgcaa   60

gctt   64

<210>   56
<211>   33
<212>   DNA
<213>   artificial sequence

<220>
<223>   oligonucleotide

<400>   56
agcttggagg ctatcatgtc gaccaagcta gca   33

<210>   57
<211>   33
<212>   DNA
<213>   artificial sequence

<220>
<223>   oligonucleotide

<400>   57
gatctgctag cttggtcgac atgatagcct cca   33

<210> 58
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 58
gatctgatat ctgcggccgc tgacgtgact cgagt   35

<210> 59
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 59
ctagactcga gtcacgtcag cggccgcaga tatca   35

<210> 60
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 60
gaagttccta ttc   13

<210> 61
<211> 8
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 61
tctagaaa   8

<210> 62
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

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<400>  62
gtataggaac ttc                                                        13


<210>  63
<211>  27
<212>  DNA
<213>  artificial sequence

<220>
<223>  oligonucleotide

<400>  63
gaagttccta ttccgaagtt cctattc                                          27


<210>  64
<211>  6
<212>  DNA
<213>  artificial sequence

<220>
<223>  oligonucleotide

<400>  64
tctaga                                                                  6


<210>  65
<211>  13
<212>  DNA
<213>  artificial sequence

<220>
<223>  oligonucleotide

<400>  65
gaagttcata ttc                                                         13


<210>  66
<211>  13
<212>  DNA
<213>  artificial sequence

<220>
<223>  oligonucleotide

<400>  66
gtatatgaac ttc                                                         13


<210>  67
<211>  13
<212>  DNA
<213>  artificial sequence
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<220>
<223> oligonucleotide

<400> 67
gaagttacta ttc   13

<210> 68
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 68
gtatagtaac ttc   13